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EQUENCE LISTING

<110> Mayfield, Stepher <120> RNA BINDING PROTEIN AND BINDING SITE USEFUL FOR EXPRESSION OF RECOMBINANT MOLECULES <130> SCR2177S <140> 09/341,550 <141> 1999-07-13 <150> PCT/US98/00840 <151> 1998-01-16 <150> 60/,035,955 <151> 1997-01-17 <150> 60/069,400 <151> 1997-12-12 <160> 14 <170> PatentIn Ver. 2.1 <210> 1 <211> 15 <212> PRT <213> Chlamydomonas reinhardtii <400> 1 Gln Tyr Gly Phe Val His Phe Glu Asp Gln Ala Ala Ala Asp Arg <210> 2 <211> 14 <212> PRT <213> Chlamydomonas reinhardtii <400> 2 Gly Phe Gly Phe Ile Asn Phe Lys Asp Ala Glu Ser Ala Ala <210> 3 <211> 32 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: oligonucleotide primer

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taggcacaaa agacctattc tagccatcaa ctttgtatcc gacgctgccg tttagctgcg 18	80
cgtcttgaag tcaagc atg gcg act act gag tcc tcg gcc ccg gcg gcc acc 23  Met Ala Thr Thr Glu Ser Ser Ala Pro Ala Ala Thr  1 5 10	32
acc cag ccg gcc agc acc ccg ctg gcg aac tcg tcg ctg tac gtc ggt 28 Thr Gln Pro Ala Ser Thr Pro Leu Ala Asn Ser Ser Leu Tyr Val Gly 15 20 25	80
gac ctg gag aag gat gtc acc gag gcc cag ctg ttc gag ctc ttc tcc 32 Asp Leu Glu Lys Asp Val Thr Glu Ala Gln Leu Phe Glu Leu Phe Ser 30 35 40	28
tcg gtt ggc cct gtg gcc tcc att cgc gtg tgc cgc gat gcc gtc acg Ser Val Gly Pro Val Ala Ser Ile Arg Val Cys Arg Asp Ala Val Thr 45 50 55 60	76
cgc cgc tcg ctg ggc tac gcc tac gtc aac tac aac agc gct ctg gac Arg Arg Ser Leu Gly Tyr Ala Tyr Val Asn Tyr Asn Ser Ala Leu Asp 65 70 75	24
ccc cag gct gct gac cgc gcc atg gag acc ctg aac tac cat gtc gtg 4' Pro Gln Ala Ala Asp Arg Ala Met Glu Thr Leu Asn Tyr His Val Val 80 85 90	72
aac ggc aag cct atg cgc atc atg tgg tcg cac cgc gac cct tcg gcc 53 Asn Gly Lys Pro Met Arg Ile Met Trp Ser His Arg Asp Pro Ser Ala 95 100 105	20
cgc aag tcg ggc gtc ggc aac atc ttc atc aag aac ctg gac aag acc Arg Lys Ser Gly Val Gly Asn Ile Phe Ile Lys Asn Leu Asp Lys Thr 110 115 120	68

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		aag Lys														808
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aag gac gac gac gtc gac gtt act gtg gtg acc gtc aag aac tgg gat Lys Asp Asp Val Asp Val Thr Val Val Thr Val Lys Asn Trp Asp 45 50 55 60	195
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		cag Gln														387
		ctc Leu														435
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		atc Ile														627
		ttc Phe														675
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atc ggt to Ile Gly Tr 30								5				
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ggt atc co								2				
att aca go Ile Thr Gl								)				
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ggt cct ta Gly Pro Ty 110								5				
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tgg atc go Trp Ile Al								2				
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ttc ggt gg Phe Gly Gl								4				
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cgt f																1010
tac t Tyr i																1058
tca Ser 270																1106
act o																1154
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gca d Ala A																1250
cgt a																1298
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gttt	attt	ta ç	gttta	ataca	ac ac	ctttt	cata	a tat	catat	cact	taat	cagct	cac o	cataç	ggcagt	1410
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	gac Asp 50															192
	tcg Ser															240
	cgc Arg															288
	ccc Pro															336
	aac Asn															384
	cgc Arg 130															432
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		ctg Leu															1008
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		gtg Val															1200
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